Typing and antibiotic resistance pattern of biofilm-producing methicillin-resistant *Staphylococcus aureus* strains with multiple drug resistance isolated from patients with urinary infection in Tehran during 2021 and 2022

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Abstract

Background: Urinary tract infections (UTIs) are one of the most common bacterial infections in humans and biofilm formation is considered one of the most important mechanisms behind the high rates of recurrence and antimicrobial resistance associated with UTIs. Methicillin-resistant *Staphylococcus aureus* (MRSA) is known as an important bacterial pathogen that can cause community and hospital-acquired urinary tract infections with a high morbidity and mortality rate. In the present study, the prevalence, antibiotic susceptibility patterns, and clonal dissemination of biofilm-producing multi-drug resistant (MDR)-MRSA strains among patients with UTI in Tehran was determined.

Materials and Methods: During 2021 and 2022 a total of 291 suspected *S. aureus* isolated from urine samples of patients with UTIs were collected from a pathobiology laboratory in Tehran, Iran, and confirmed using polymerase chain reaction (PCR) by specific primers for the *nuc*A gene. The ability of strains to produce biofilm was evaluated using quantitative microtiter plate (MTP) and qualitative Congo red agar (CRA) methods. The susceptibility of biofilm-producing strains to cefoxitin was determined by the guidelines of the Clinical and Laboratory Standards Institute (CLSI) and MRSA strains were tested for resistance to 16 antibiotics using the disk diffusion method. Moreover, the minimum inhibitory concentrations (MICs) of oxacillin and vancomycin were measured using E-test. A combination of PhP typing, prophage typing, Staphylococcal cassette chromosome *mec* (SCC*mec*) typing, *agr* typing, and the Phene Plate (PhP), and *ccr* typing was employed for the typing of biofilm-producing MRSA strains.

Results: In this study, all strains were confirmed as *S. aureus* and 105 strains (36%) were selected as biofilm producers, in which 66% (n=57) of strains were resistant to methicillin and carried the *mec*A gene. All strains showed resistance to 8-13 antibiotics and were classified as MDR strains. Resistance to penicillin G, erythromycin, ciprofloxacin, tobramycin, clindamycin, and amikacin was 100%; and, none of the strains showed resistance to vancomycin, linezolid, chloramphenicol and quinupristin-dalfopristin. A total of 21 PhP types consisting of 7 common types (CTs) and 14 single types (STs) were also found among biofilm-producing MRSA strains, in which CT2 and CT1 were the most prevalent types. Also, SCC*mec* types I-III, types 1-3 *ccr*, 4 prophage types (SGB, SGF, SGFa, and SGFb), and 2 prophage patterns were determined which confirmed the hospital origin of MRSA strains.

Conclusion: The results of the present study revealed the high prevalence of biofilm-producing MDR-MRSA strains among patients with UTI in Tehran. These strains were hospital-acquired and potentially were able to produce a broad range of virulence factors that could be a major public health concern in Tehran, which highlighted the importance of proper implementation and practice of policies and procedures on infection control and prevention (ICP) to minimize the clonal dissemination of such strains from hospitals to the community.

Keywords: Urinary infection, MRSA, biofilm, typing, Congo red agar, microtiter plate, multi-drug resistance

Importance, prevalence, and clinical manifestations of human papillomavirus infection in children and adolescents

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Abstract

Human papillomavirus is clinically important due to the fact that it could affect people of all ages, including children and adolescents. Despite its well-established role in adults, particularly in the development of cervical cancer, the impact of HPV on young populations remains unknown. In recent years, several studies have been conducted to identify and diagnose this infection in children and adolescents. This study reviewed the prevalence, clinical manifestations, and routes of HPV transmission in children and adolescents. According to the studies conducted, this study shows a significant prevalence of HPV DNA in the pediatric population, with diverse clinical manifestations such as verruca vulgaris, anogenital warts, and recurrent adolescent respiratory papillomatosis, through vertical transmission from mother to child as well as horizontal transmission. Given the characteristics of this virus and its unique functions in oncogenicity, it seems rational to improve management strategies and pave the way for future research in pediatric diseases for HPV infection and clinical approaches.

Evaluation of the nitric oxide effectiveness against biofilm-producing methicillin-resistant *Staphylococcus aureus* strains isolated from patients with urinary tract infections in Tehran during 2021-2023

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Abstract

Background and purpose: Methicillin-resistant *Staphylococcus aureus* (MRSA) has been confirmed to play an important role in urinary tract infections (UTIs). The biofilm formation is responsible for the survival and persistence of these strains in the urinary system which can result in the recurrence of infection. The purpose of the present study was to evaluate the effectiveness of different concentrations of nitric oxide (NO) on the biofilm of uropathogenic MRSA isolates from patients with UTI in Tehran during 2021-2023.

وMaterials and Methods: During 2 years, a total of 318 suspected *S. aureus* isolates were collected from patients with UTI in a referral hospital in Tehran, and were identified using polymerase chain reaction (PCR) by specific primers for *nuc*A genes. The resistance of these strains to methicillin was determined by the combination of agar screening and disk diffusion methods as recommended by the Clinical and Laboratory Standards Institute. Qualitative Congo red agar (CRA) and quantitative microtiter plate (MTP) assays were employed to assess the ability of strains to form biofilm. The frequency of genes involved in biofilm formation including *ica*A, *ica*D, *clf*A, *fnbp*A, and *cna* genes was detected by separate PCR tests and also the prevalence of different staphylococcal cassette chromosome *mec* (SCC*mec*) types among these strains was evaluated using the multiplex-PCR tests. The resistance of biofilm producers to 14 antibiotics was examined using the CLSI guidelines. Moreover, the effectiveness of 30 µM and 125 nM of sodium nitroprusside (SNP) on inhibiting biofilm formation and disintegrating preformed biofilms was evaluated.

Results: Totally, 297 strains (93%) were identified as *S. aureus*, of which 30% (90 strains) were resistant to methicillin and harbored the *mec*A gene. Also, 72% of strains could form a biofilm, and the prevalence of *ica*A, *ica*D, *clf*A, *fnbp*A, and *cna* genes was 89, 86, 75, 72, and 58%, respectively. Moreover, 26 and 74% of strains were classified as community acquired-MRSA (CA-MRSA) (positive for SCC*mec* types IV and V) and hospital acquired-MRSA (HA-MRSA) (harbored SCC*mec* types I-III), and resistance to penicillin, ciprofloxacin, erythromycin, clindamycin, gentamicin, tetracycline, and rifampin was 100, 74, 72, 68, 66, 63 and 62%, respectively. The 30 µM concentration of SNP significantly affected the biofilm formation and biofilm dispersal.

Conclusion: The results of the present study indicate the prevalence of biofilm-producing MRSA strains among patients with UTI in Tehran. Without appropriate infection prevention and control programs, this issue could escalate into a significant public health concern within our country. On the other hand, the high concentration of SNP significantly decreased the biofilm formation and increased biofilm dispersal among these strains. Thus, SNP could be considered a potential strategy to mitigate the spread of these strains in healthcare settings.

Keywords: Urinary tract infection, biofilm, MRSA, sodium nitroprusside, nitric oxide

Investigation of demographic characteristics, risk factors, symptoms, complications and prognosis of the patients with botulism who hospitalized in Valiasr Hospital, Zanjan in 1391-1401

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Abstract

Introduction: Foodborne botulism is a potentially fatal form of food poisoning most commonly caused by consuming improperly canned or preserved vegetables, fruits, dairy products, or fish. Botulism is one of most important public health problems in the world and especially in Iran. This study aimed to investigate the epidemiology of foodborne botulism in Zanjan Province, Iran.

Methods: This study is a descriptive cross-sectional research design. The target population was patients admitted to Valiasr Hospital in Zanjan with botulism from 2012 to 2022. We collected data on demographic characteristics, risk factors for infection, recent history of botulism in close relatives, clinical manifestations, paraclinical findings, and prognosis by reviewing the medical records of hospitalized patients.

Result: In the present study, 54 individuals diagnosed with botulism were examined. The study found that most patients with botulism were middle-aged, male, urban residents, and had a history of infections in their families. The suspected food was the most common risk factor among botulism patients, with local dairy products being the most frequently consumed food source. Visual disturbances, diplopia, and ophthalmoplegia were the most common symptoms of botulism, while ocular, neurological, respiratory, gastrointestinal complications, and intubation were identified as the most prevalent clinical complications in botulism patients.

Conclusion: Suspicious food posed the most significant risk factor for botulism patients, with local dairy products being the most commonly consumed contaminated source. Public health education campaigns, ensuring sufficient heat during food consumption, and avoiding unpasteurized dairy products could effectively prevent the occurrence of this dangerous foodborne illness.

Keywords: Botulism, risk factor, food poisoning, clinical complications, laboratory complications

The Role of Pneumococcal Vaccination in Altering Circulating Serotypes in the Community: Risk or Benefit

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Abstract

Streptococcus pneumoniae is one of the most important causes of severe respiratory and systemic infections in both children and adults, characterized by over 100 diverse capsular serotypes that pose significant challenges for control and prevention. Pneumococcal conjugate vaccines (PCVs) have played a pivotal role in public health by substantially reducing the prevalence of vaccine-covered serotypes and associated antibiotic resistance. However, the phenomenon of serotype replacement and the emergence of non-vaccine serotypes with increased pathogenicity and resistance threaten the long-term efficacy of these vaccines. This article aimed to evaluate the impact of vaccination on pneumococcal serotype distribution and its epidemiological implications by analyzing existing evidence on serotype dynamics, antibiotic resistance trends, and the imperative for ongoing serotype surveillance and vaccine reformulation. The findings suggest that, alongside enhancing vaccine coverage and accessibility among high-risk populations, the development of next-generation vaccines with broader serotype coverage and enhanced mucosal and systemic immunity is crucial for effective pneumococcal disease control and mitigation of risks associated with serotype shifts.

Keywords: Vaccination, Serotype, Streptococcus pneumoniae, Children